

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/735,863

Source: _____

Date Processed by STIC: _____

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 12/01/2004

PATENT APPLICATION: US/10/735,863

TIME: 12:33:43

Input Set : N:\Crf3\RULE60\10735863.raw.txt

Output Set: N:\CRF4\12012004\J735863.raw

1 <110> APPLICANT: Brettman, Lee R.
 2 Fox, Judith A.
 3 Allison, David Edward
 4 <120> TITLE OF INVENTION: Method of Administering an Antibody
 5 <130> FILE REFERENCE: 1855.2007-001
 6 <140> CURRENT APPLICATION NUMBER: US/10/735,863
 7 <141> CURRENT FILING DATE: 2003-12-15
 8 <150> PRIOR APPLICATION NUMBER: US/09/748,960
 9 <151> PRIOR FILING DATE: 2000-12-27
 10 <150> PRIOR APPLICATION NUMBER: US 09/550,082
 11 <151> PRIOR FILING DATE: 2000-04-14
 12 <160> NUMBER OF SEQ ID NOS: 16
 13 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 396
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Mus musculus
 19 <220> FEATURE:
 20 <221> NAME/KEY: CDS
 21 <222> LOCATION: (1)...(396)
 22 <400> SEQUENCE: 1

23	atg aag ttg cct gtt agg ctg ttg gtg ctt ctg ttg ttc tgg att cct	48
24	Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Phe Trp Ile Pro	
25	1 5 10 15	
26	gtt tcc gga ggt gat gtt gtg gtg act caa act cca ctc tcc ctg cct	96
27	Val Ser Gly Gly Asp Val Val Val Thr Gln Thr Pro Leu Ser Leu Pro	
28	20 25 30	
29	gtc agc ttt gga gat caa gtt tct atc tct tgc agg tct agt cag agt	144
30	Val Ser Phe Gly Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser	
31	35 40 45	
32	ctt gca aag agt tat ggg aac acc tat ttg tct tgg tac ctg cac aag	192
33	Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu His Lys	
34	50 55 60	
35	cct ggc cag tct cca cag ctc atc tat ggg att tcc aac aga ttt	240
36	Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe	
37	65 70 75 80	
38	tct ggg gtg cca gac agg ttc agt ggc agt ggt tca ggg aca gat ttc	288
39	Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
40	85 90 95	
41	aca ctc aag atc agc aca ata aag cct gag gac ttg gga atg tat tac	336
42	Thr Leu Lys Ile Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr	
43	100 105 110	
44	tgc tta caa ggt aca cat cag ccg tac acg ttc gga ggg acc aag	384

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45 Cys Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly Gly Thr Lys
 46 115 120 125 396
 47 ctg gaa ata aaa
 48 Leu Glu Ile Lys
 49 130
 51 <210> SEQ ID NO: 2
 52 <211> LENGTH: 132
 53 <212> TYPE: PRT
 54 <213> ORGANISM: Mus musculus
 55 <220> FEATURE:
 56 <221> NAME/KEY: SIGNAL
 57 <222> LOCATION: (1)...(20)
 58 <223> OTHER INFORMATION: signal peptide
 59 <220> FEATURE:
 60 <221> NAME/KEY: SITE
 61 <222> LOCATION: (21)...(43)
 62 <223> OTHER INFORMATION: framework 1
 63 <220> FEATURE:
 64 <221> NAME/KEY: SITE
 65 <222> LOCATION: (44)...(59)
 66 <223> OTHER INFORMATION: CDR1
 67 <220> FEATURE:
 68 <221> NAME/KEY: SITE
 69 <222> LOCATION: (60)...(74)
 70 <223> OTHER INFORMATION: framework 2
 71 <220> FEATURE:
 72 <221> NAME/KEY: SITE
 73 <222> LOCATION: (75)...(81)
 74 <223> OTHER INFORMATION: CDR2
 75 <220> FEATURE:
 76 <221> NAME/KEY: SITE
 77 <222> LOCATION: (82)...(113)
 78 <223> OTHER INFORMATION: framework 3
 79 <220> FEATURE:
 80 <221> NAME/KEY: SITE
 81 <222> LOCATION: (114)...(122)
 82 <223> OTHER INFORMATION: CDR3
 83 <220> FEATURE:
 84 <221> NAME/KEY: SITE
 85 <222> LOCATION: (123)...(132)
 86 <223> OTHER INFORMATION: framework 4
 87 <400> SEQUENCE: 2
 88 Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Leu Phe Trp Ile Pro
 89 1 5 10 15
 90 Val Ser Gly Gly Asp Val Val Val Thr Gln Thr Pro Leu Ser Leu Pro
 91 20 25 30
 92 Val Ser Phe Gly Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser
 93 35 40 45
 94 Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu His Lys

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95      50          55          60
96 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe
97      65          70          75          80
98 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
99      85          90          95
100     Thr Leu Lys Ile Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr
101      100         105         110
102     Cys Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly Gly Thr Lys
103      115         120         125
104     Leu Glu Ile Lys
105      130
107 <210> SEQ ID NO: 3
108 <211> LENGTH: 420
109 <212> TYPE: DNA
110 <213> ORGANISM: Mus musculus
111 <220> FEATURE:
112 <221> NAME/KEY: CDS
113 <222> LOCATION: (1)...(420)
114 <400> SEQUENCE: 3
115 atg gga tgg agc tgt atc atc ctc ttc ttg gta tca aca gct aca agt      48
116 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ser Thr Ala Thr Ser
117      1           5           10          15
118 gtc cac tcc cag gtc caa ctg cag cag cct ggg gct gag ctt gtg aag      96
119 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
120      20          25          30
121 cct ggg act tca gtg aag ctg tcc tgc aag ggt tat ggc tac acc ttc      144
122 Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly Tyr Gly Tyr Thr Phe
123      35          40          45
124 acc agc tac tgg atg cac tgg gtg aag cag agg cct gga caa ggc ctt      192
125 Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
126      50          55          60
127 gag tgg atc gga gag att gat cct tct gag agt aat act aac tac aat      240
128 Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
129      65          70          75          80
130 caa aaa ttc aag ggc aag gcc aca ttg act gta gac att tcc tcc agc      288
131 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser
132      85          90          95
133 aca gcc tac atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc      336
134 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
135      100         105         110
136 tac tat tgt gca aga ggg ggt tac gac gga tgg gac tat gct att gac      384
137 Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
138      115         120         125
139 tac tgg ggt caa ggc acc tca gtc acc gtc tcc tca
140 Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
141      130         135         140
143 <210> SEQ ID NO: 4
144 <211> LENGTH: 140
145 <212> TYPE: PRT

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146 <213> ORGANISM: Mus musculus
 147 <220> FEATURE:
 148 <221> NAME/KEY: SIGNAL
 149 <222> LOCATION: (1)...(19)
 150 <223> OTHER INFORMATION: signal peptide
 151 <220> FEATURE:
 152 <221> NAME/KEY: SITE
 153 <222> LOCATION: (20)...(49)
 154 <223> OTHER INFORMATION: framework 1
 155 <220> FEATURE:
 156 <221> NAME/KEY: SITE
 157 <222> LOCATION: (50)...(54)
 158 <223> OTHER INFORMATION: CDR1
 159 <220> FEATURE:
 160 <221> NAME/KEY: SITE
 161 <222> LOCATION: (55)...(68)
 162 <223> OTHER INFORMATION: framework 2
 163 <220> FEATURE:
 164 <221> NAME/KEY: SITE
 165 <222> LOCATION: (69)...(85)
 166 <223> OTHER INFORMATION: CDR2
 167 <220> FEATURE:
 168 <221> NAME/KEY: SITE
 169 <222> LOCATION: (86)...(117)
 170 <223> OTHER INFORMATION: framework 3
 171 <220> FEATURE:
 172 <221> NAME/KEY: SITE
 173 <222> LOCATION: (118)...(129)
 174 <223> OTHER INFORMATION: CDR3
 175 <220> FEATURE:
 176 <221> NAME/KEY: SITE
 177 <222> LOCATION: (130)...(140)
 178 <223> OTHER INFORMATION: framework 4
 179 <400> SEQUENCE: 4
 180 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ser Thr Ala Thr Ser
 181 1 5 10 15
 182 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 183 20 25 30
 184 Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly Tyr Gly Tyr Thr Phe
 185 35 40 45
 186 Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 187 50 55 60
 188 Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
 189 65 70 75 80
 190 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser
 191 85 90 95
 192 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 193 100 105 110
 194 Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp

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195	115	120	125
196	Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser		
197	130	135	140
199	<210> SEQ ID NO: 5		
200	<211> LENGTH: 540		
201	<212> TYPE: DNA		
202	<213> ORGANISM: Artificial Sequence		
203	<220> FEATURE:		
204	<223> OTHER INFORMATION: Portion of the heavy chain of LDP-02 with a heavy		
205	chain signal peptide		
206	<220> FEATURE:		
207	<221> NAME/KEY: CDS		
208	<222> LOCATION: (1)...(540)		
209	<400> SEQUENCE: 5		
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211	Met Lys Cys Thr Trp Val Ile Leu Phe Leu Val Ser Thr Ala Thr Ser		
212	1 5 10 15		
213	gtc cac tcc cag gtc caa cta gtg cag tct ggg gct gag gtt aag aag	96	
214	Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys		
215	20 25 30		
216	cct ggg gct tca gtg aag gtg tcc tgc aag ggt tct ggc tac acc ttc	144	
217	Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe		
218	35 40 45		
219	acc agc tac tgg atg cat tgg gtg agg cag gcg cct ggc caa cgt cta	192	
220	Thr Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu		
221	50 55 60		
222	gag tgg atc gga gag att gat cct tct gag agt aat act aac tac aat	240	
223	Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn		
224	65 70 75 80		
225	caa aaa ttc aag gga cgc gtc aca ttg act gta gac att tcc gct agc	288	
226	Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Ile Ser Ala Ser		
227	85 90 95		
228	aca gcc tac atg gag ctc agc agc ctg aga tct gag gac act gcg gtc	336	
229	Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val		
230	100 105 110		
231	tac tat tgt gca aga ggg ggt tac gac gga tgg gac tat gct att gac	384	
232	Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp		
233	115 120 125		
234	tac tgg ggt caa ggc acc ctg gtc acc gtc tcc tca gcc tcc acc aag	432	
235	Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys		
236	130 135 140		
237	ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg	480	
238	Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly		
239	145 150 155 160		
240	ggc aca gca ggc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg	528	
241	Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro		
242	165 170 175		
243	gtg acg gtg tcg	540	
244	Val Thr Val Ser		

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10735863.raw.txt

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